

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2017/08/14 14:39:35*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/home/bethany/projects/planctomycetes+halococci/QC/Gem_JW3-
8s0.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

Command line:	blasr ../pacbraw/F05_1/Analysis_Results/m150527_152142_42153_c100830882550000001823183611251585_s1_p0.bas.h5 ../assembly/final_contigs/Gem_JW3-8s0_final_contigs.fasta --sam --out Gem_JW3-8s0.sam --nproc 16
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	1 (5.3.574e1c2)
Analysis date:	Mon Aug 14 14:31:56 NZST 2017
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/bethany/projects/planctomycetes+halococci/QC/Gem_JW3-8s0.sorted.bam

## 2. Summary

### 2.1. Globals

Reference size	10,148,538
Number of reads	254,225
Mapped reads	254,225 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	0 / 0%
Read min/max/mean length	49 / 36,230 / 7,125.35
Duplicated reads (estimated)	42,580 / 16.75%
Duplication rate	7.59%
Clipped reads	254,224 / 100%

### 2.2. ACGT Content

Number/percentage of A's	164,487,339 / 18.51%
Number/percentage of C's	271,250,887 / 30.53%
Number/percentage of T's	164,923,274 / 18.56%
Number/percentage of G's	270,953,736 / 30.49%
Number/percentage of N's	0 / 0%
GC Percentage	61.02%

### 2.3. Coverage

Mean	90.877
Standard Deviation	35.7822

### 2.4. Mapping Quality

Mean Mapping Quality	228.55
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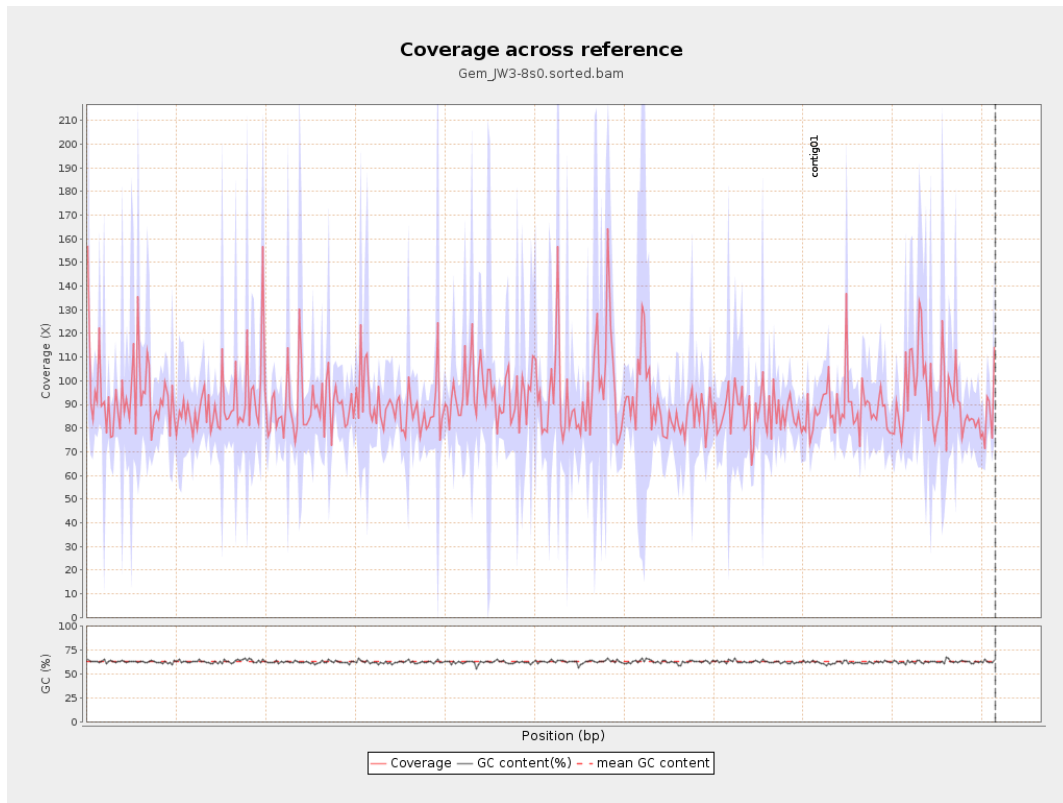
## 2.5. Mismatches and indels

General error rate	17.67%
Insertions	80,594,192
Mapped reads with at least one insertion	99.83%
Deletions	30,708,713
Mapped reads with at least one deletion	98.96%
Homopolymer indels	17.72%

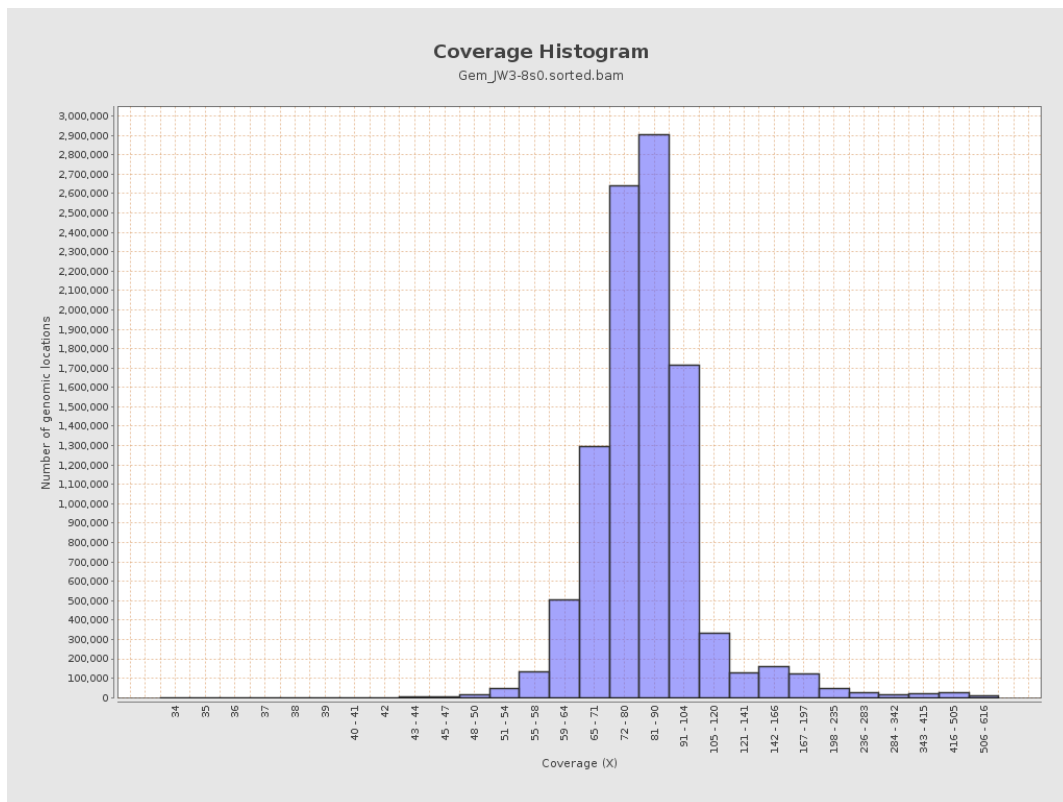
## 2.6. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
contig01	10148538	922268413	90.877	35.7822

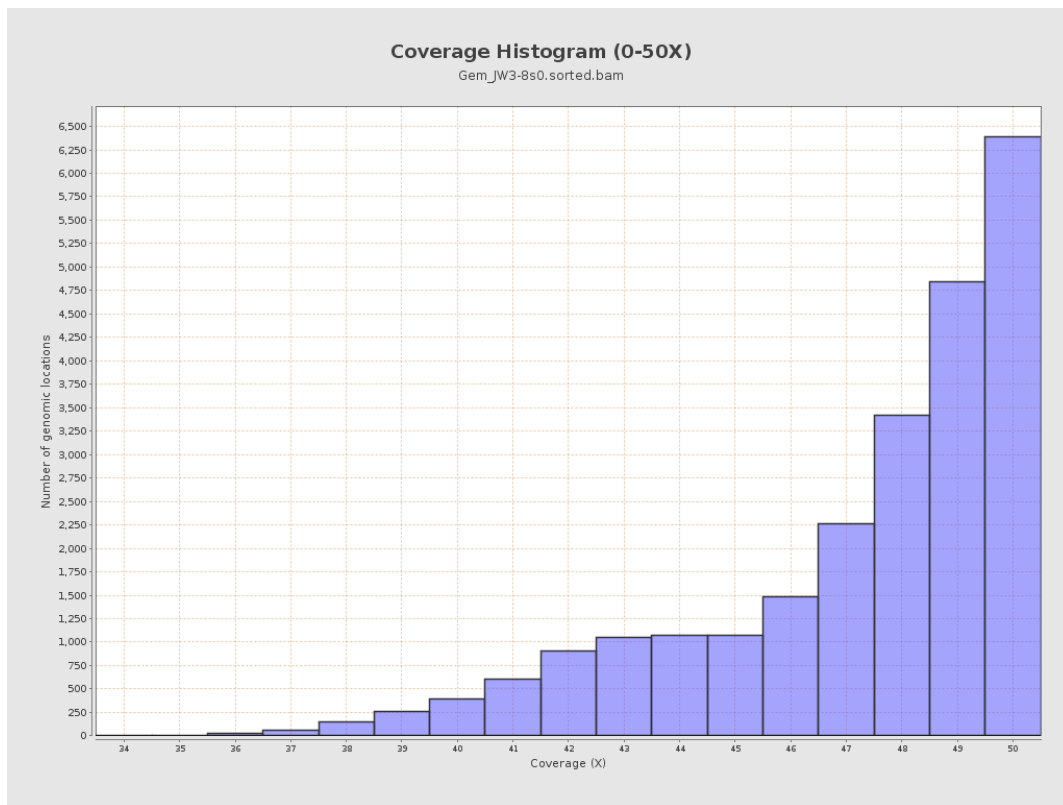
### 3. Results : Coverage across reference



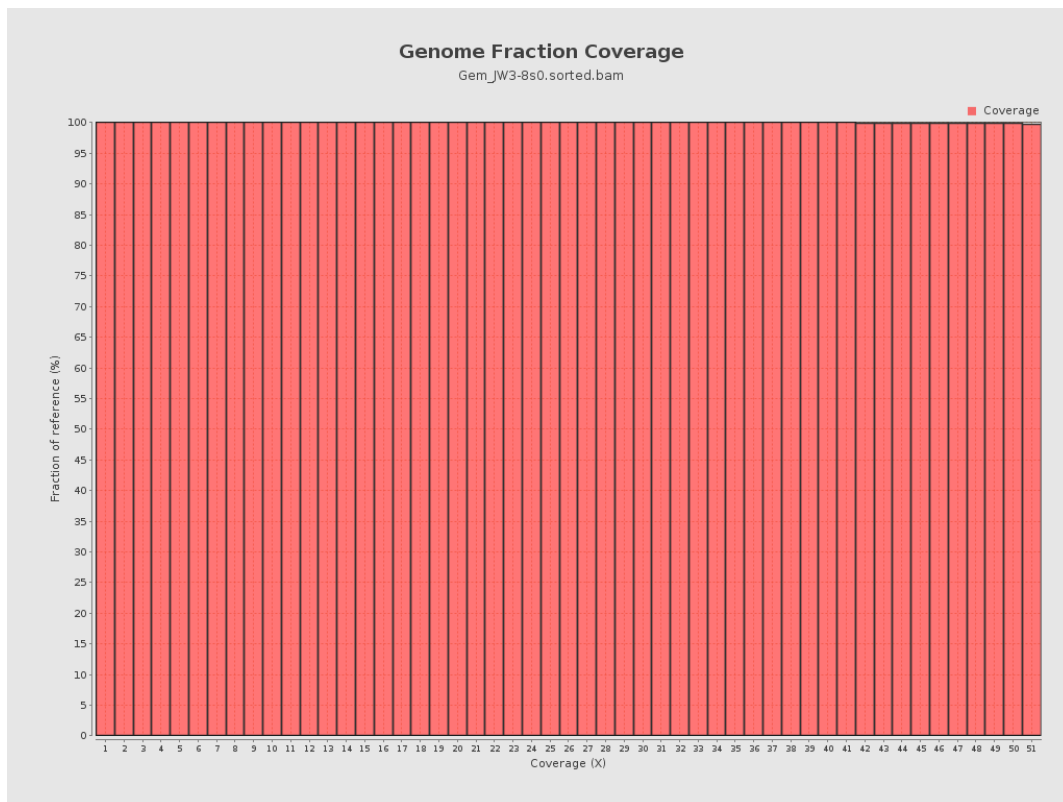
## 4. Results : Coverage Histogram



## 5. Results : Coverage Histogram (0-50X)

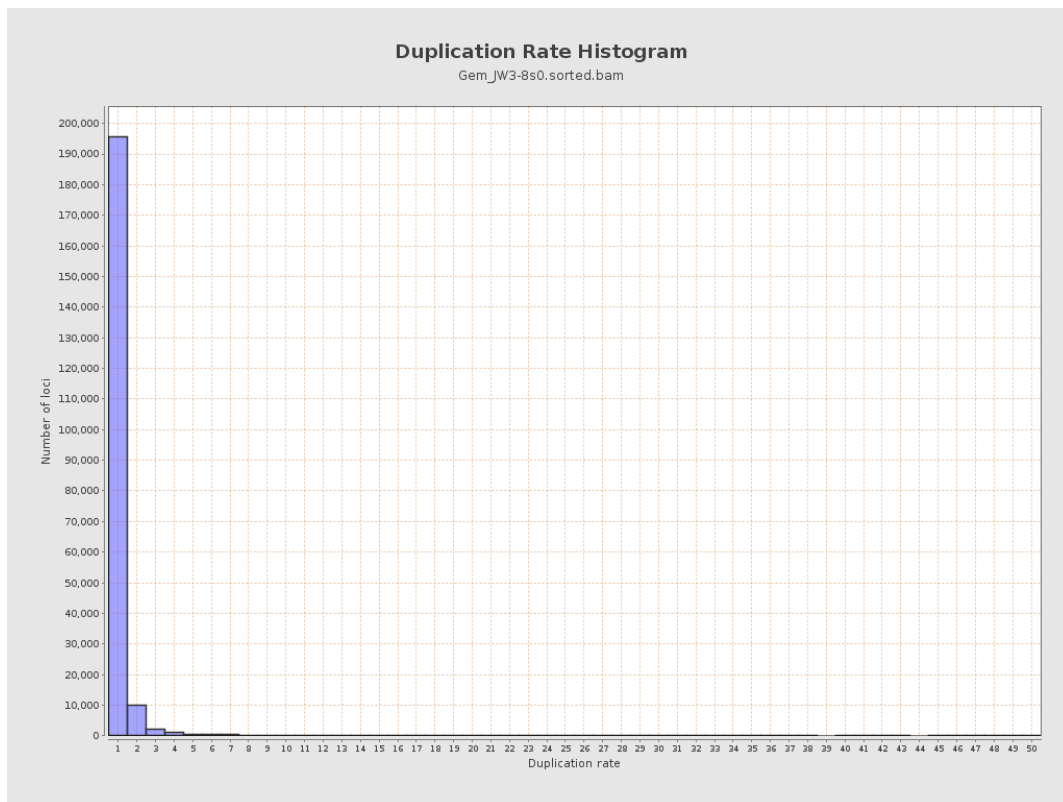


## 6. Results : Genome Fraction Coverage

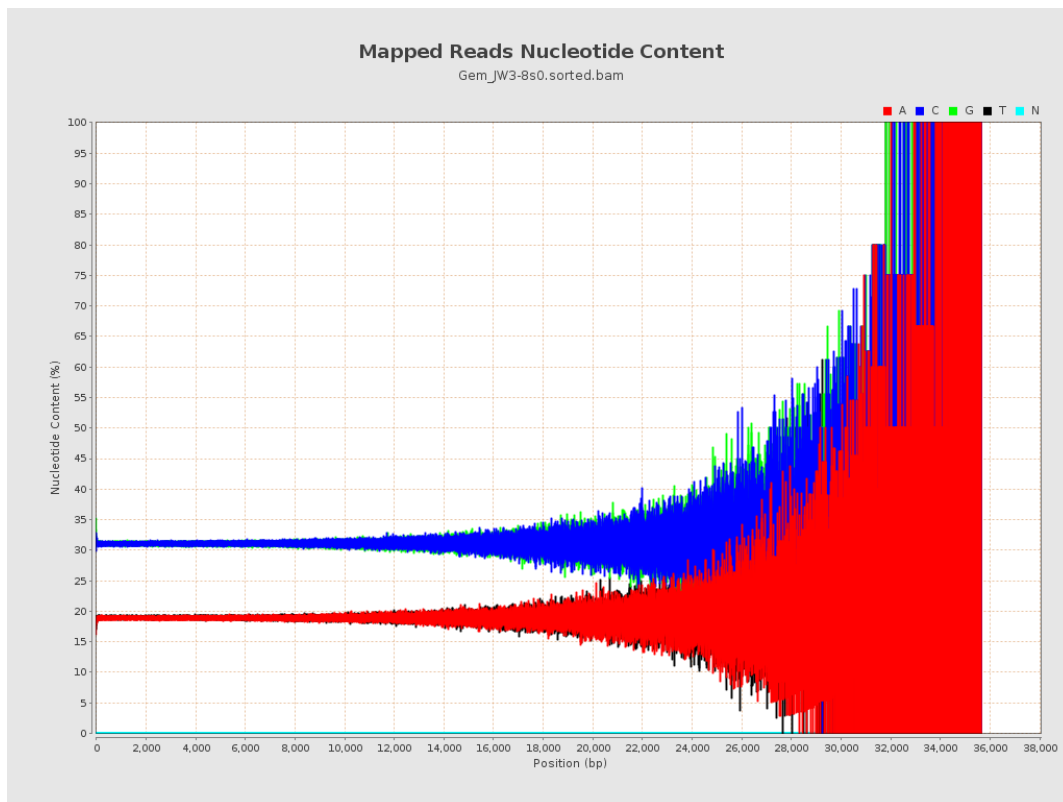




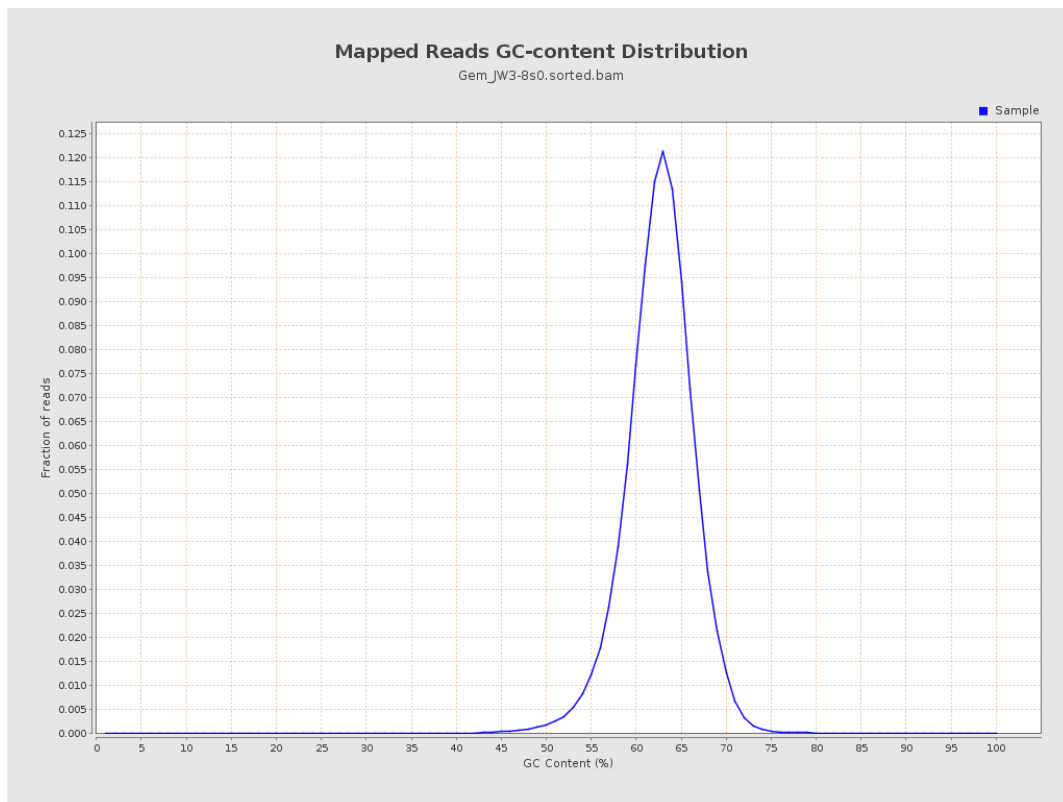
## 7. Results : Duplication Rate Histogram



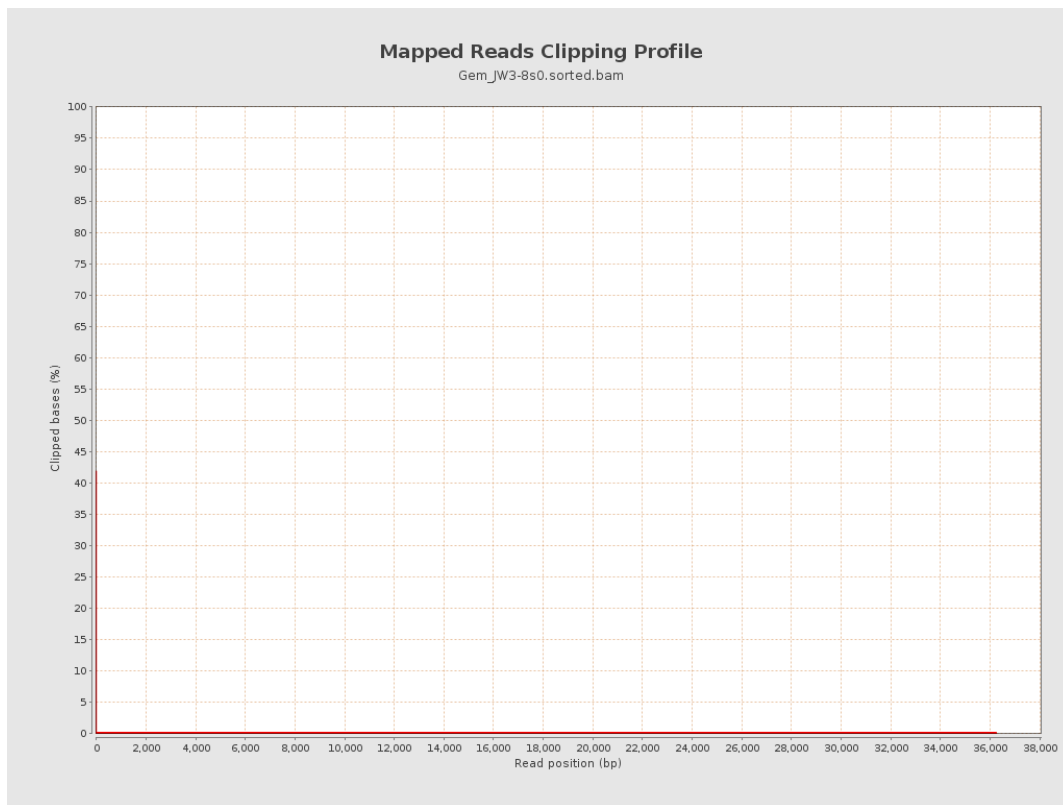
## 8. Results : Mapped Reads Nucleotide Content



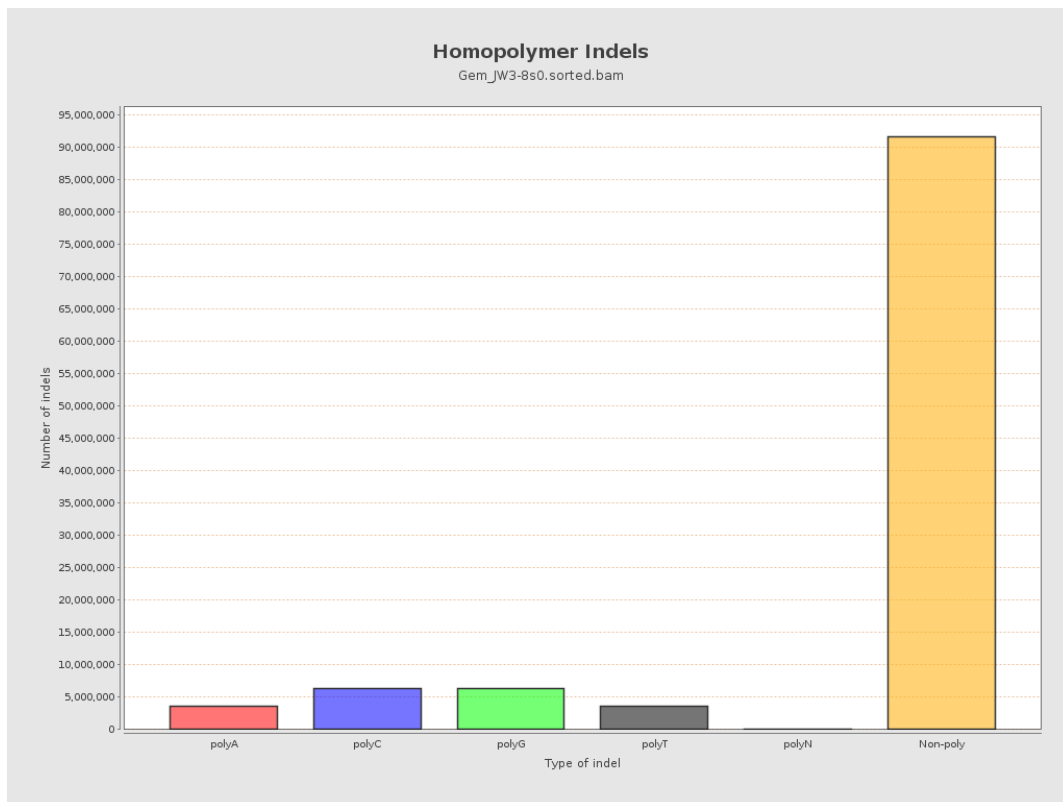
## 9. Results : Mapped Reads GC-content Distribution



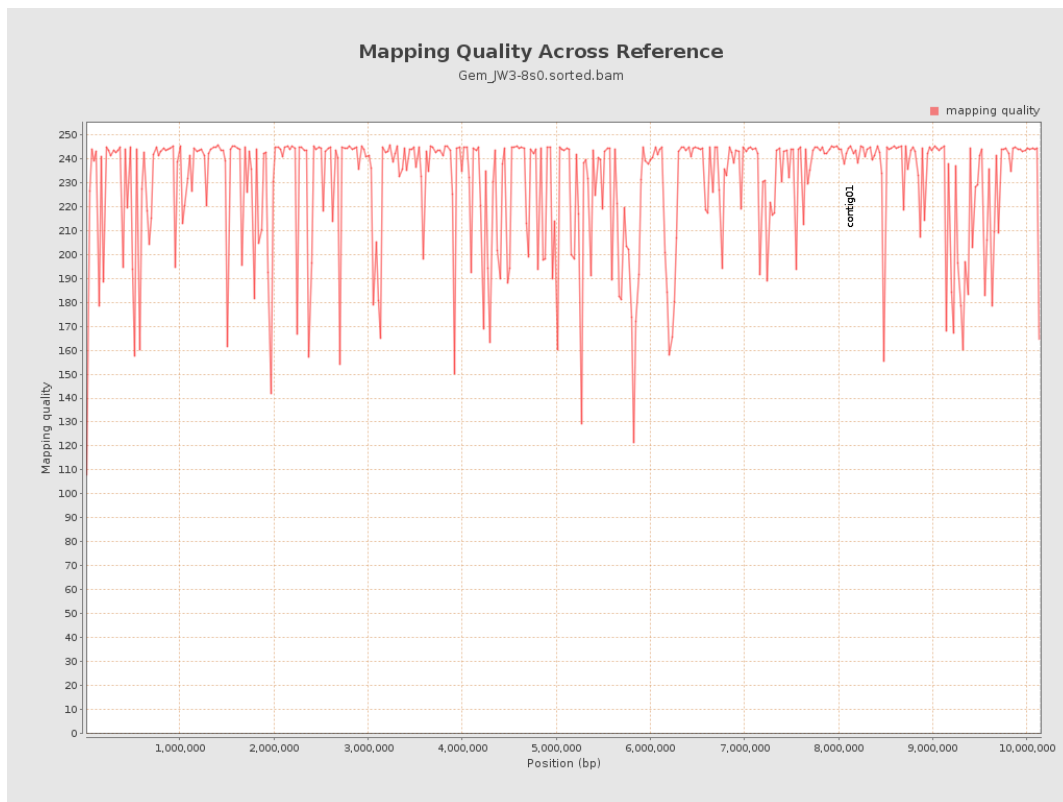
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

